

SEQUENCE LISTING

<110> Russell, William
Klaenhammer, Todd

<120> LACTOBACILLUS BETA-GLUCURONIDASE AND DNA ENCODING THE SAME

<130> 5051.514

<150> 60/206,372

<151> 2000-05-23

<160> 14

<170> PatentIn version 3.0

<210> 1

<211> 2150

<212> DNA

<213> Lactobacillus gasseri

<220>

<221> CDS

<222> (153)..(1946)

<400> 1

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agagaaaaca ttactagaaa ggaaaatcat ct atg gaa tct gca cta tat cca      173
                               Met Glu Ser Ala Leu Tyr Pro
                               1                               5
att caa aat aaa tat cgg ttt aac act tta atg aat ggc act tgg caa      221
Ile Gln Asn Lys Tyr Arg Phe Asn Thr Leu Met Asn Gly Thr Trp Gln
          10                      15                      20
ttt gaa act gat cct aac tct gtt ggt ctt gac gag gga tgg aat aaa      269
Phe Glu Thr Asp Pro Asn Ser Val Gly Leu Asp Glu Gly Trp Asn Lys
          25                      30                      35
gag ttg cct gat cct gaa gaa atg cct gta cca ggt acg ttt gca gaa      317
Glu Leu Pro Asp Pro Glu Glu Met Pro Val Pro Gly Thr Phe Ala Glu
          40                      45                      50                      55
tta act act aag cga gac cgt aaa tac tat act gga gac ttt tgg tat      365
Leu Thr Thr Lys Arg Asp Arg Lys Tyr Tyr Thr Gly Asp Phe Trp Tyr
          60                      65                      70
caa aaa gac ttc ttt att cct tca ttt cta aag aag aaa gaa ctt tat      413
Gln Lys Asp Phe Phe Ile Pro Ser Phe Leu Lys Lys Lys Glu Leu Tyr
          75                      80                      85
atc cgt ttt ggt tcg gtt act cat cgc gca aaa gta ttt att aat gga      461
Ile Arg Phe Gly Ser Val Thr His Arg Ala Lys Val Phe Ile Asn Gly
          90                      95                      100
cat gaa gtc ggt caa cat gaa ggt ggt ttt tta cca ttt caa gta aaa      509
His Glu Val Gly Gln His Glu Gly Gly Phe Leu Pro Phe Gln Val Lys

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105	110	115	
att tca aat tat att aat tac gac caa act aat cgt gta act gtt tta Ile Ser Asn Tyr Ile Asn Tyr Asp Gln Thr Asn Arg Val Thr Val Leu 120 125 130 135			557
gtc aat aac gaa tta tct gaa aaa gct att cct tgc ggc acc gaa gaa Val Asn Asn Glu Leu Ser Glu Lys Ala Ile Pro Cys Gly Thr Glu Glu 140 145 150			605
atc tta gat aac ggt caa aaa ctt gct caa cct tat ttt gat ttc ttc Ile Leu Asp Asn Gly Gln Lys Leu Ala Gln Pro Tyr Phe Asp Phe Phe 155 160 165			653
aat tat tct ggc att atg cgg aat gtc tgg ctc tta gca ctt cct caa Asn Tyr Ser Gly Ile Met Arg Asn Val Trp Leu Leu Ala Leu Pro Gln 170 175 180			701
agc caa atc act aat ttt aaa cta aat tat caa tta gca aat aat aag Ser Gln Ile Thr Asn Phe Lys Leu Asn Tyr Gln Leu Ala Asn Asn Lys 185 190 195			749
gca aca att acc tac aat atc gag gca aat aat aat gct gaa ttt aaa Ala Thr Ile Thr Tyr Asn Ile Glu Ala Asn Asn Ala Glu Phe Lys 200 205 210 215			797
gta aca ctt ttc gat aat caa aaa gaa gta gcg tgt gct act tct aaa Val Thr Leu Phe Asp Asn Gln Lys Glu Val Ala Cys Ala Thr Ser Lys 220 225 230			845
aat act agt agt tta aca att aag aat ccg cac ctt tgg agt cca aac Asn Thr Ser Ser Leu Thr Ile Lys Asn Pro His Leu Trp Ser Pro Asn 235 240 245			893
gat ccg tat tca tac aaa ata aag att gaa atg ctc gaa gac gga aaa Asp Pro Tyr Ser Tyr Lys Ile Lys Ile Glu Met Leu Glu Asp Gly Lys 250 255 260			941
aca gtt gac gaa tac aca gat aaa att ggt atc cgc aca gtt aaa att Thr Val Asp Glu Tyr Thr Asp Lys Ile Gly Ile Arg Thr Val Lys Ile 265 270 275			989
gtg aat gat aaa atc ttg ctc aat aat cac cca att tat tta aaa ggc Val Asn Asp Lys Ile Leu Leu Asn Asn His Pro Ile Tyr Leu Lys Gly 280 285 290 295			1037
ttt ggc aag cac gaa gat ttt aat gtt tta ggc aaa gca gtt aac gaa Phe Gly Lys His Glu Asp Phe Asn Val Leu Gly Lys Ala Val Asn Glu 300 305 310			1085
agc att atc aaa cgc gac tac gaa tgc atg aaa tgg att ggc gct aac Ser Ile Ile Lys Arg Asp Tyr Glu Cys Met Lys Trp Ile Gly Ala Asn 315 320 325			1133
tgt ttt aga agc agt cac tat cct tac gcc gaa gaa tgg tat caa tat Cys Phe Arg Ser Ser His Tyr Pro Tyr Ala Glu Glu Trp Tyr Gln Tyr 330 335 340			1181
gcc gat aaa tat ggc ttt tta att att gat gaa gta ccc gct gtt ggt Ala Asp Lys Tyr Gly Phe Leu Ile Ile Asp Glu Val Pro Ala Val Gly 345 350 355			1229
ctt aat cgt tca ata act aac ttt ctt aat gta act aat tct aat cag Leu Asn Arg Ser Ile Thr Asn Phe Leu Asn Val Thr Asn Ser Asn Gln 360 365 370 375			1277

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tcg cac ttt ttt gct tcg aaa act gtg cct gaa tta aaa aag gtc cat	1325
Ser His Phe Phe Ala Ser Lys Thr Val Pro Glu Leu Lys Lys Val His	
380 385 390	
gaa caa gaa ata aaa gaa atg atc gat cgc gac cag cgt cac cct tca	1373
Glu Gln Glu Ile Lys Glu Met Ile Asp Arg Asp Gln Arg His Pro Ser	
395 400 405	
gtg att gcc tgg agt tta ttc aat gaa cca gaa tca act act caa gaa	1421
Val Ile Ala Trp Ser Leu Phe Asn Glu Pro Glu Ser Thr Thr Gln Glu	
410 415 420	
tcc tat gac tat ttc aaa gat att ttt gcc ttt gcg aga aaa ttg gat	1469
Ser Tyr Asp Tyr Phe Lys Asp Ile Phe Ala Phe Ala Arg Lys Leu Asp	
425 430 435	
cca caa aat cgt cct tat act gga act tta gtt atg ggt agc ggt cca	1517
Pro Gln Asn Arg Pro Tyr Thr Gly Thr Leu Val Met Gly Ser Gly Pro	
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aaa gtg gat aag ctt cac cca ctt tgt gac ttt gtc tgc tta aac cgt	1565
Lys Val Asp Lys Leu His Pro Leu Cys Asp Phe Val Cys Leu Asn Arg	
460 465 470	
tat tat ggt tgg tac gtt gct ggt ggt cct gaa atc gtt aat gct aaa	1613
Tyr Tyr Gly Trp Tyr Val Ala Gly Gly Pro Glu Ile Val Asn Ala Lys	
475 480 485	
aag atg ctg gaa gat gaa cta gac ggc tgg caa aac tta aag ctt aat	1661
Lys Met Leu Glu Asp Glu Leu Asp Gly Trp Gln Asn Leu Lys Leu Asn	
490 495 500	
aaa cca ttt gtc ttt act gag ttt ggc gct gat aca tta tct tct tct	1709
Lys Pro Phe Val Phe Thr Glu Phe Gly Ala Asp Thr Leu Ser Ser Ser	
505 510 515	
cat cgc ctt cca gat gaa atg tgg agc caa gaa tat caa aat gaa tat	1757
His Arg Leu Pro Asp Glu Met Trp Ser Gln Glu Tyr Gln Asn Glu Tyr	
520 525 530 535	
tat caa atg tat ttt gat ata ttt aag aaa tat cca ttt att tgt ggc	1805
Tyr Gln Met Tyr Phe Asp Ile Phe Lys Lys Tyr Pro Phe Ile Cys Gly	
540 545 550	
gaa tta gtt tgg aac ttt gct gac ttt aag acg agt gaa gga atc atg	1853
Glu Leu Val Trp Asn Phe Ala Asp Phe Lys Thr Ser Glu Gly Ile Met	
555 560 565	
cgt gtt ggt ggt aac gat aaa gga att ttt act cgc gat cgt gaa cct	1901
Arg Val Gly Gly Asn Asp Lys Gly Ile Phe Thr Arg Asp Arg Glu Pro	
570 575 580	
aaa gat att gcc ttt acc ttg aaa aag aga tgg caa caa tta aat	1946
Lys Asp Ile Ala Phe Thr Leu Lys Lys Arg Trp Gln Gln Leu Asn	
585 590 595	
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tcatttgata tcgattatatt gattatgggc gcgatttttt attgattttg ataataattt	2066
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<210> 2
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 <213> Lactobacillus gasseri

<400> 2

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Leu Asp Glu Gly Trp Asn Lys Glu Leu Pro Asp Pro Glu Glu Met Pro
          35          40          45

Val Pro Gly Thr Phe Ala Glu Leu Thr Thr Lys Arg Asp Arg Lys Tyr
          50          55          60

Tyr Thr Gly Asp Phe Trp Tyr Gln Lys Asp Phe Phe Ile Pro Ser Phe
65          70          75          80

Leu Lys Lys Lys Glu Leu Tyr Ile Arg Phe Gly Ser Val Thr His Arg
          85          90          95

Ala Lys Val Phe Ile Asn Gly His Glu Val Gly Gln His Glu Gly Gly
          100          105          110

Phe Leu Pro Phe Gln Val Lys Ile Ser Asn Tyr Ile Asn Tyr Asp Gln
          115          120          125

Thr Asn Arg Val Thr Val Leu Val Asn Asn Glu Leu Ser Glu Lys Ala
          130          135          140

Ile Pro Cys Gly Thr Glu Glu Ile Leu Asp Asn Gly Gln Lys Leu Ala
145          150          155          160

Gln Pro Tyr Phe Asp Phe Phe Asn Tyr Ser Gly Ile Met Arg Asn Val
          165          170          175

Trp Leu Leu Ala Leu Pro Gln Ser Gln Ile Thr Asn Phe Lys Leu Asn
          180          185          190

Tyr Gln Leu Ala Asn Asn Lys Ala Thr Ile Thr Tyr Asn Ile Glu Ala
          195          200          205

Asn Asn Asn Ala Glu Phe Lys Val Thr Leu Phe Asp Asn Gln Lys Glu
          210          215          220

Val Ala Cys Ala Thr Ser Lys Asn Thr Ser Ser Leu Thr Ile Lys Asn
225          230          235          240

Pro His Leu Trp Ser Pro Asn Asp Pro Tyr Ser Tyr Lys Ile Lys Ile
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Glu Met Leu Glu Asp Gly Lys Thr Val Asp Glu Tyr Thr Asp Lys Ile
          260          265          270

Gly Ile Arg Thr Val Lys Ile Val Asn Asp Lys Ile Leu Leu Asn Asn
          275          280          285

His Pro Ile Tyr Leu Lys Gly Phe Gly Lys His Glu Asp Phe Asn Val
          290          295          300

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Leu	Gly	Lys	Ala	Val	Asn	Glu	Ser	Ile	Ile	Lys	Arg	Asp	Tyr	Glu	Cys	305	310	315	320
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Ala	Glu	Glu	Trp	Tyr	Gln	Tyr	Ala	Asp	Lys	Tyr	Gly	Phe	Leu	Ile	Ile	340	345	350	
Asp	Glu	Val	Pro	Ala	Val	Gly	Leu	Asn	Arg	Ser	Ile	Thr	Asn	Phe	Leu	355	360	365	
Asn	Val	Thr	Asn	Ser	Asn	Gln	Ser	His	Phe	Phe	Ala	Ser	Lys	Thr	Val	370	375	380	
Pro	Glu	Leu	Lys	Lys	Val	His	Glu	Gln	Glu	Ile	Lys	Glu	Met	Ile	Asp	385	390	395	400
Arg	Asp	Gln	Arg	His	Pro	Ser	Val	Ile	Ala	Trp	Ser	Leu	Phe	Asn	Glu	405	410	415	
Pro	Glu	Ser	Thr	Thr	Gln	Glu	Ser	Tyr	Asp	Tyr	Phe	Lys	Asp	Ile	Phe	420	425	430	
Ala	Phe	Ala	Arg	Lys	Leu	Asp	Pro	Gln	Asn	Arg	Pro	Tyr	Thr	Gly	Thr	435	440	445	
Leu	Val	Met	Gly	Ser	Gly	Pro	Lys	Val	Asp	Lys	Leu	His	Pro	Leu	Cys	450	455	460	
Asp	Phe	Val	Cys	Leu	Asn	Arg	Tyr	Tyr	Gly	Trp	Tyr	Val	Ala	Gly	Gly	465	470	475	480
Pro	Glu	Ile	Val	Asn	Ala	Lys	Lys	Met	Leu	Glu	Asp	Glu	Leu	Asp	Gly	485	490	495	
Trp	Gln	Asn	Leu	Lys	Leu	Asn	Lys	Pro	Phe	Val	Phe	Thr	Glu	Phe	Gly	500	505	510	
Ala	Asp	Thr	Leu	Ser	Ser	Ser	His	Arg	Leu	Pro	Asp	Glu	Met	Trp	Ser	515	520	525	
Gln	Glu	Tyr	Gln	Asn	Glu	Tyr	Tyr	Gln	Met	Tyr	Phe	Asp	Ile	Phe	Lys	530	535	540	
Lys	Tyr	Pro	Phe	Ile	Cys	Gly	Glu	Leu	Val	Trp	Asn	Phe	Ala	Asp	Phe	545	550	555	560
Lys	Thr	Ser	Glu	Gly	Ile	Met	Arg	Val	Gly	Gly	Asn	Asp	Lys	Gly	Ile	565	570	575	
Phe	Thr	Arg	Asp	Arg	Glu	Pro	Lys	Asp	Ile	Ala	Phe	Thr	Leu	Lys	Lys	580	585	590	
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